

BLAST

Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Protein Sequence (21 letters)

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

Description

None

Molecule type

amino acid

Query Length

21

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Related Structures](#)
[Multiple alignment](#) [NEW](#)

Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Dec 10, 2009 5:41 PM
Number of letters	3,463,213,929
Number of sequences	10,157,076

Entrez query none

Karlin-Altschul statistics

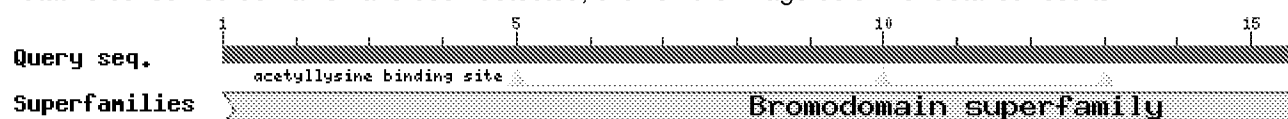
Params	Ungapped	Gapped
Lambda	0.332117	0.294
K	0.27808	0.11
H	1.83624	0.61

Results Statistics

Length adjustment	11
Effective length of query	10
Effective length of database	3351486093
Effective search space	33514860930
Effective search space used	33514860930

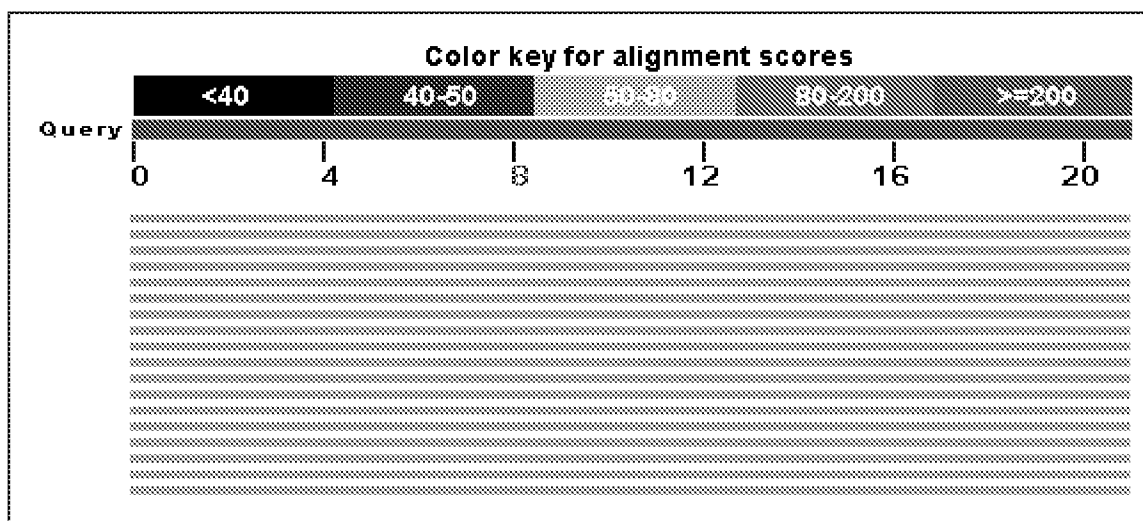
[Graphic Summary](#)[Show Conserved Domains](#)

Putative conserved domains have been detected, click on the image below for detailed results.

**Distribution of 104 Blast Hits on the Query Sequence**

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



1. The first step in the process is to identify the problem or goal. This involves understanding the current situation and what needs to be achieved.

2. Next, it is important to gather relevant information and data. This can be done through research, interviews, or observation.

3. Once the information is gathered, the next step is to analyze it. This involves looking for patterns, trends, and potential causes.

4. After analysis, the next step is to develop a plan or strategy. This should outline the steps needed to achieve the goal.

5. The final step is to implement the plan. This involves putting the strategy into action and monitoring progress.



Descriptions

		Score	
E		(Bits)	Value
Sequences producing significant alignments:			
pdb 3GG3 A	Chain A, Crystal Structure Of The Bromodomain Of H...	69.8	3e-11
ref XP_002194393.1	PREDICTED: p300/CBP-associated factor [Ta...	69.8	3e-11
ref XP_001493774.2	PREDICTED: p300/CBP-associated factor [Eq...	69.8	3e-11
ref XP_001508358.1	PREDICTED: similar to PCAF [Ornithorhynch...	69.8	3e-11
gb EDL82853.1	p300/CBP-associated factor, isoform CRA_b [Rat...	69.8	3e-11
gb EDL82852.1	p300/CBP-associated factor, isoform CRA_a [Rat...	69.8	3e-11
gb EDL23666.1	p300/CBP-associated factor, isoform CRA_b [Mus...	69.8	3e-11
gb EDL23665.1	p300/CBP-associated factor, isoform CRA_a [Mus...	69.8	3e-11
ref XP_001380514.1	PREDICTED: similar to p300/CBP-associated...	69.8	3e-11
ref XP_613744.3	PREDICTED: p300/CBP-associated factor [Bos t...	69.8	3e-11
gb EAW64305.1	p300/CBP-associated factor, isoform CRA_a [Hom...	69.8	3e-11
gb EAW64306.1	p300/CBP-associated factor, isoform CRA_b [Hom...	69.8	3e-11
ref XP_426001.2	PREDICTED: similar to PCAF [Gallus gallus]	69.8	3e-11
ref XP_516321.2	PREDICTED: p300/CBP-associated factor [Pan t...	69.8	3e-11
ref XP_001086807.1	PREDICTED: similar to p300/CBP-associated...	69.8	3e-11
db EAE59136.1	PCAF [Gallus gallus]	69.8	3e-11
gb AAC50890.2	p300/CBP-associated factor [Homo sapiens]	69.8	3e-11
gb AAF70498.1 AF254442.1	PCAF acetyltransferase [Mus musculus]	69.8	3e-11
ref XP_534249.2	PREDICTED: similar to p300/CBP-associated fa...	69.8	3e-11
ref NP_064389.2	K(lysine) acetyltransferase 2B [Mus musculus...	69.8	3e-11
ref NP_003875.3	K(lysine) acetyltransferase 2B [Homo sapiens...	69.8	3e-11
db EAE33658.1	unnamed protein product [Mus musculus]	69.8	3e-11
pdb 1N72 A	Chain A, Structure And Ligand Of A Histone Acetyl...	69.8	3e-11
ref NP_001019423.1	K(lysine) acetyltransferase 2B [Rattus no...	66.0	5e-10
gb EDL05223.1	mCG4405 [Mus musculus]	65.5	6e-10
ref XP_911230.1	PREDICTED: similar to P300/CBP-associated fa...	65.5	6e-10
ref XP_284106.1	PREDICTED: similar to P300/CBP-associated fa...	65.5	6e-10
ref NP_001038499.1	K(lysine) acetyltransferase 2B [Danio rer...	59.6	4e-08
emb CAF99403.1	unnamed protein product [Tetraodon nigroviridis]	59.6	4e-08
pdb 3D7C A	Chain A, Crystal Structure Of The Bromodomain Of H...	54.9	1e-06
ref XP_001495139.2	PREDICTED: similar to GCN5 general contro...	54.9	1e-06
ref XP_001922732.1	PREDICTED: im:7156024 [Danio rerio]	54.9	1e-06
gb EDL02540.1	GCN5 general control of amino acid synthesis-1...	54.9	1e-06
gb EDL02538.1	GCN5 general control of amino acid synthesis-1...	54.9	1e-06
gb EAW60801.1	GCN5 general control of amino-acid synthesis 5...	54.9	1e-06
gb EAW60802.1	GCN5 general control of amino-acid synthesis 5...	54.9	1e-06
ref XP_511500.2	PREDICTED: GCN5 general control of amino-aci...	54.9	1e-06
ref XP_001166738.1	PREDICTED: GCN5 general control of amino-...	54.9	1e-06
ref NP_001100520.1	general control of amino acid synthesis 5...	54.9	1e-06
ref XP_001094333.1	PREDICTED: similar to GCN5 general contro...	54.9	1e-06
gb AAR03834.1	general control of amino-acid synthesis 5-like...	54.9	1e-06
gb AAH03983.1	Kat2a protein [Mus musculus]	54.9	1e-06
pdb 1F68 A	Chain A, Nmr Solution Structure Of The Bromodomain...	54.9	1e-06
gb AAC50641.1	GCN5 [Homo sapiens]	54.9	1e-06

ref XP_860469.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_860436.1	PREDICTED: similar to General control of ami...	54.9	1e-06
ref XP_860364.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_860401.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_849978.1	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
ref XP_548094.2	PREDICTED: similar to GCN5 general control o...	54.9	1e-06
gb AAE50690.1	hGCN5=transcriptional adaptor [human, testis, ...	54.9	1e-06
ref NP_066564.2	general control of amino acid synthesis 5-li...	54.9	1e-06
dbj BAE29392.1	unnamed protein product [Mus musculus]	54.9	1e-06
dbj BAE26296.1	unnamed protein product [Mus musculus]	54.9	1e-06
dbj BAE33207.1	unnamed protein product [Mus musculus]	54.9	1e-06
ref NP_064388.2	general control of amino acid synthesis 5-li...	54.9	1e-06
ref NP_001033099.1	general control of amino acid synthesis 5...	54.9	1e-06
sp Q9JRD2.1	KAT2A_MOUSE RecName: Full=Histone acetyltransfera...	54.9	1e-06
gb AAC39769.1	hGCN5 [Homo sapiens]	54.9	1e-06
ref XP_001515022.1	PREDICTED: similar to GCN5 general contro...	54.5	1e-06
ref XP_002194616.1	PREDICTED: GCN5 general control of amino-...	52.8	4e-06
emb CAG92829.1	unnamed protein product [Tetraodon nigroviridis]	52.8	4e-06
ref NP_989660.1	general control of amino acid synthesis 5-li...	52.8	4e-06
ref XP_002123196.1	PREDICTED: similar to K(lysine) acetyltra...	51.1	1e-05
gb EFA10157.1	hypothetical protein TcasGA2_TC012345 [Triboli...	48.6	8e-05
ref XP_002427469.1	fetal alzheimer antigen, falz, putative [...	48.6	8e-05
ref XP_001811424.1	PREDICTED: similar to fetal alzheimer ant...	48.6	8e-05
ref XP_001985459.1	GH14490 [Drosophila grimshawi] >gb EDV978...	46.0	5e-04
ref XP_001605087.1	PREDICTED: similar to fetal alzheimer ant...	44.8	0.001
ref XP_395718.3	PREDICTED: similar to Enhancer of bithorax C...	44.8	0.001
ref XP_002092960.1	GE21036 [Drosophila yakuba] >gb EDW92692....	44.3	0.002
ref XP_001970994.1	GG14675 [Drosophila erecta] >gb EDV50020....	44.3	0.002
gb AAL16644.1	AF417921.1 nucleosome remodeling factor large s...	44.3	0.002
ref NP_728503.1	enhancer of bithorax, isoform B [Drosophila ...	44.3	0.002
ref NP_728507.1	enhancer of bithorax, isoform A [Drosophila ...	44.3	0.002
ref XP_0021117619.1	predicted protein [Trichoplax adhaerens] ...	43.9	0.002
ref XP_002341883.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_002341882.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_002151156.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_002151155.1	histone acetyltransferase (Gcn5), putativ...	43.5	0.003
ref XP_001352486.2	GA16840 [Drosophila pseudoobscura pseudoo...	43.5	0.003
ref XP_002026084.1	GL16133 [Drosophila persimilis] >gb EDW33...	43.5	0.003
ref XP_001956111.1	GF24755 [Drosophila ananassae] >gb EDV389...	43.5	0.003
ref XP_002062665.1	GK17657 [Drosophila willistoni] >gb EDW73...	43.1	0.004
ref XP_002060306.1	GJ16047 [Drosophila virilis] >gb EDW57119...	43.1	0.004
ref XP_001983171.1	GH15750 [Drosophila grimshawi] >gb EDV955...	43.1	0.004
ref XP_002627606.1	histone acetyltransferase GCN5 [Ajellomyc...	42.6	0.005
ref XP_316196.4	AGAP006133-PA [Anopheles gambiae str. PEST] ...	42.6	0.005
ref XP_002383268.1	histone acetyltransferase (Gcn5), putativ...	42.2	0.007
ref XP_001389241.1	hypothetical protein An01g08160 [Aspergil...	42.2	0.007
ref XP_001266775.1	histone acetyltransferase (Gcn5), putativ...	42.2	0.007
ref XP_001272118.1	histone acetyltransferase (Gcn5), putativ...	42.2	0.007


ref XP_001212327.1	histone acetyltransferase GCN5 [Aspergill...	42.2	0.007
ref XP_001816805.1	hypothetical protein [Aspergillus oryzae ...	42.2	0.007
ref XP_751566.1	histone acetyltransferase (Gcn5) [Aspergillu...	42.2	0.007
gb EER24293.1	histone acetyltransferase GCN5, putative [Cocc...	41.8	0.009
ref XP_002541088.1	histone acetyltransferase GCN5 [Uncinocar...	41.8	0.009
gb EEW45435.1	histone acetyltransferase GCN5 [Paracoccidioid...	41.8	0.009
gb EEW36638.1	histone acetyltransferase GCN5 [Paracoccidioid...	41.8	0.009
gb EEW20829.1	histone acetyltransferase GCN5 [Paracoccidioid...	41.8	0.009

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)

>**pdb|3GG3|A**  Chain A, Crystal Structure Of The Bromodomain Of Human Pcaf
pdb|3GG3|B  Chain B, Crystal Structure Of The Bromodomain Of Human Pcaf
 Length=119

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEIVIRSPM 21
 FMEPVKRTEAPGYEIVIR PM
 Sbjct 36 FMEPVKRTEAPGYEIVIRFPM 56

>**ref|XP_002194393.1|**  PREDICTED: p300/CBP-associated factor [Taeniopygia gutt
 Length=742

GENE ID: 100227387 LOC100227387 | p300/CBP-associated factor
 [Taeniopygia guttata]

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEIVIRSPM 21
 FMEPVKRTEAPGYEIVIR PM
 Sbjct 658 FMEPVKRTEAPGYEIVIRFPM 678

>**ref|XP_001493774.2|**  PREDICTED: p300/CBP-associated factor [Equus caballus]
 Length=784

GENE ID: 100061976 KAT2B | K(lysine) acetyltransferase 2B [Equus caballus]

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEIVIRSPM 21
 FMEPVKRTEAPGYEIVIR PM
 Sbjct 700 FMEPVKRTEAPGYEIVIRFPM 720

>**ref|XP_001508358.1|**  PREDICTED: similar to PCAF [Ornithorhynchus anatinus]
 Length=817

GENE ID: 100077074 LOC100077074 | similar to PCAF [Ornithorhynchus anatinus]

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEIVIRSPM 21
 FMEPVKRTEAPGYEIVIR PM
 Sbjct 733 FMEPVKRTEAPGYEIVIRFPM 753

>**gb|EDL82853.1|**  p300/CBP-associated factor, isoform CRA_b [Rattus norvegicus]
 Length=704

GENE ID: 301164 Pcaf | p300/CBP-associated factor [Rattus norvegicus]
 (10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEIVIRSPM 21
FMEPVKRTEAPGYEIVIR PM
Sbjct 620 FMEPVKRTEAPGYEIVIRFPM 640

>**gb|EDL82852.1** |  p300/CBP-associated factor, isoform CRA_a [Rattus norvegicus]
Length=731

GENE ID: 301164 Pcaf | p300/CBP-associated factor [Rattus norvegicus]
(10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEIVIRSPM 21
FMEPVKRTEAPGYEIVIR PM
Sbjct 647 FMEPVKRTEAPGYEIVIRFPM 667

>**gb|EDL23666.1** |  p300/CBP-associated factor, isoform CRA_b [Mus musculus]
Length=706

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEIVIRSPM 21
FMEPVKRTEAPGYEIVIR PM
Sbjct 622 FMEPVKRTEAPGYEIVIRFPM 642

>**gb|EDL23665.1** |  p300/CBP-associated factor, isoform CRA_a [Mus musculus]
Length=746

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEIVIRSPM 21
FMEPVKRTEAPGYEIVIR PM
Sbjct 662 FMEPVKRTEAPGYEIVIRFPM 682

>**ref|XP_001380514.1** |  PREDICTED: similar to p300/CBP-associated factor, [Mono domestica]
Length=966

GENE ID: 100031193 LOC100031193 | similar to p300/CBP-associated factor
[Monodelphis domestica]

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYEIVIRSPM 21
FMEPVKRTEAPGYEIVIR PM
Sbjct 882 FMEPVKRTEAPGYEIVIRFPM 902


>**ref|XP_613744.3** |  PREDICTED: p300/CBP-associated factor [Bos taurus]
Length=826

GENE ID: 407215 KAT2B | K(lysine) acetyltransferase 2B [Bos taurus]

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYEIVIRSPM 21
FMEPVKRTEAPGYEIVIR PM


Sbjct 742 FMEPVKRTEAPGYEYEVIRFPM 762

>gb|EAW64305.1|  p300/CBP-associated factor, isoform CRA_a [Homo sapiens]
Length=825

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]
(Over 100 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 741 FMEPVKRTEAPGYEYEVIRFPM 761

>gb|EAW64306.1|  p300/CBP-associated factor, isoform CRA_b [Homo sapiens]
Length=768

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]
(Over 100 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 741 FMEPVKRTEAPGYEYEVIRFPM 761

>ref|XP_426001.2|  PREDICTED: similar to PCAF [Gallus gallus]
Length=753

GENE ID: 428441 PCAF | p300/CBP-associated factor [Gallus gallus]
(10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 669 FMEPVKRTEAPGYEYEVIRFPM 689

>ref|XP_516321.2|  PREDICTED: p300/CBP-associated factor [Pan troglodytes]
Length=806

GENE ID: 460219 KAT2B | K(lysine) acetyltransferase 2B [Pan troglodytes]

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 722 FMEPVKRTEAPGYEYEVIRFPM 742

>ref|XP_001086807.1|  PREDICTED: similar to p300/CBP-associated factor [Macac]
Length=858

GENE ID: 698283 LOC698283 | similar to p300/CBP-associated factor
[Macaca mulatta]

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 774 FMEPVKRTEAPGYEYEVIRFPM 794

>dbj|BAB59138.1|  PCAF [Gallus gallus]
Length=760

GENE ID: 428441 PCAF | p300/CBP-associated factor [Gallus gallus]
(10 or fewer PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 676 FMEPVKRTEAPGYEYEVIRFPM 696

>**gb|AAC50890.2** |  p300/CBP-associated factor [Homo sapiens]
Length=832

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]
(Over 100 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 748 FMEPVKRTEAPGYEYEVIRFPM 768

>**gb|AAF70498.1|AF254442_1**  PCAF acetyltransferase [Mus musculus]
Length=813

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 729 FMEPVKRTEAPGYEYEVIRFPM 749


>**ref|XP_534249.2** |  PREDICTED: similar to p300/CBP-associated factor [Canis fa
Length=760





GENE ID: 477052 KAT2B | K(lysine) acetyltransferase 2B [Canis lupus familiaris]

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 676 FMEPVKRTEAPGYEYEVIRFPM 696

>**ref|NP_064389.2** |  K(lysine) acetyltransferase 2B [Mus musculus]





sp|Q9JHD1.2|KAT2B_MOUSE  RecName: Full=Histone acetyltransferase KAT2B; AltName: acetyltransferase 2B; AltName: Full=Histone acetyltransferase PCAF; Short=Histone acetylase PCAF; AltName: Full=P300/CBP-associated factor; Short=P/CAF

gb|AAH82581.1 |  K(lysine) acetyltransferase 2B [Mus musculus]
gb|EDL23667.1 |  p300/CBP-associated factor, isoform CRA_c [Mus musculus]
gb|AAI45897.1 |  K(lysine) acetyltransferase 2B [Mus musculus]
gb|AAI38196.1 |  K(lysine) acetyltransferase 2B [Mus musculus]
Length=813

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
(Over 10 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSPM 21
FMEPVKRTEAPGYEYEVIR PM
Sbjct 729 FMEPVKRTEAPGYEYEVIRFPM 749

>ref|NP_003875.3|  K(lysine) acetyltransferase 2B [Homo sapiens]
 sp|Q92831.3|KAT2B_HUMAN  RecName: Full=Histone acetyltransferase KAT2B; AltName: acetyltransferase 2B; AltName: Full=Histone acetyltransferase PCAF; Short=Histone acetylase PCAF; AltName: Full=P300/CBP-associated factor; Short=P/CAF
 gb|AAH60823.1|  K(lysine) acetyltransferase 2B [Homo sapiens]
 gb|AAH70075.1|  K(lysine) acetyltransferase 2B [Homo sapiens]
 dbj|BAI45566.1| K(lysine) acetyltransferase 2B [synthetic construct]
 Length=832

GENE ID: 8850 KAT2B | K(lysine) acetyltransferase 2B [Homo sapiens]
 (Over 100 PubMed links)

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)








Query 1 FMEPVKRTEAPGYEIVIRSPM 21
 FMEPVKRTEAPGYEIVIR PM
 Sbjct 748 FMEPVKRTEAPGYEIVIRFPM 768

>dbj|BAE33658.1|  unnamed protein product [Mus musculus]
 Length=813

GENE ID: 18519 Kat2b | K(lysine) acetyltransferase 2B [Mus musculus]
 (Over 10 PubMed links)



Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYEIVIRSPM 21
 FMEPVKRTEAPGYEIVIR PM
 Sbjct 729 FMEPVKRTEAPGYEIVIRFPM 749

>pdb|1N72|A  Chain A, Structure And Ligand Of A Histone Acetyltransferase Bromodomain
 pdb|1JM4|B  Chain B, Nmr Structure Of PCAF BROMODOMAIN IN COMPLEX WITH HIV-1 Tat Peptide
 pdb|1WUG|A  Chain A, Complex Structure Of Pcaf Bromodomain With Small Chemic Ligand Np1
 pdb|1WUM|A  Chain A, Complex Structure Of Pcaf Bromodomain With Small Chemic Ligand Np2
 pdb|1ZS5|A  Chain A, Structure-Based Evaluation Of Selective And Non-Selecti Small Molecules That Block Hiv-1 Tat And Pcaf Association
 pdb|2RNW|A  Chain A, The Structural Basis For Site-Specific Lysine-Acetylate Histone Recognition By The Bromodomains Of The Human Transcriptional Co-Activators Pcaf And Cbp
 pdb|2RNX|A  Chain A, The Structural Basis For Site-Specific Lysine-Acetylate Histone Recognition By The Bromodomains Of The Human Transcriptional Co-Activators Pcaf And Cbp
 Length=118

Score = 69.8 bits (157), Expect = 3e-11
 Identities = 20/21 (95%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

Query 1 FMEPVKRTEAPGYEIVIRSPM 21
 FMEPVKRTEAPGYEIVIR PM
 Sbjct 34 FMEPVKRTEAPGYEIVIRFPM 54

>ref|NP_001019423.1|  K(lysine) acetyltransferase 2B [Rattus norvegicus]
 gb|AAH92639.1|  P300/CBP-associated factor [Rattus norvegicus]
 Length=84

GENE ID: 301164 Pcaf | p300/CBP-associated factor [Rattus norvegicus]
 (10 or fewer PubMed links)

Score = 66.0 bits (148), Expect = 5e-10


Identities = 19/20 (95%), Positives = 19/20 (95%), Gaps = 0/20 (0%)

```
Query  2    MEPVKRTEAPGYEYEVIRSPM  21
          MEPVKRTEAPGYEYEVIR  PM
Sbjct  1    MEPVKRTEAPGYEYEVIRFPM  20
```

>**gb|EDL05223.1|** mCG4405 [Mus musculus]
Length=813

Score = 65.5 bits (147), Expect = 6e-10
Identities = 19/21 (90%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


```
Query  1    FMEPVKRTEAPGYEYEVIRSPM  21
          F+EPVKRTEAPGYEYEVIR  PM
Sbjct  729  FLEPVKRTEAPGYEYEVIRFPM  749
```

>**ref|XP_911230.1|**  PREDICTED: similar to P300/CBP-associated factor [Mus musculus]
Length=829

GENE ID: 330129 Gm5109 | predicted gene 5109 [Mus musculus]

Score = 65.5 bits (147), Expect = 6e-10
Identities = 19/21 (90%), Positives = 20/21 (95%), Gaps = 0/21 (0%)


```
Query  1    FMEPVKRTEAPGYEYEVIRSPM  21
          F+EPVKRTEAPGYEYEVIR  PM
Sbjct  745  FLEPVKRTEAPGYEYEVIRFPM  765
```


>**ref|XP_284106.1|**  PREDICTED: similar to P300/CBP-associated factor [Mus musculus]
Length=829

GENE ID: 330129 Gm5109 | predicted gene 5109 [Mus musculus]

Score = 65.5 bits (147), Expect = 6e-10
Identities = 19/21 (90%), Positives = 20/21 (95%), Gaps = 0/21 (0%)

```
Query  1    FMEPVKRTEAPGYEYEVIRSPM  21
          F+EPVKRTEAPGYEYEVIR  PM
Sbjct  745  FLEPVKRTEAPGYEYEVIRFPM  765
```

>**ref|NP_001038499.1|**  K(lysine) acetyltransferase 2B [Danio rerio]

emb|CAK04378.1|  novel protein similar to vertebrate p300/CBP-associated factor (PCAF) [Danio rerio]
Length=796

GENE ID: 563942 kat2b | K(lysine) acetyltransferase 2B [Danio rerio]
(10 or fewer PubMed links)


Score = 59.6 bits (133), Expect = 4e-08
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)


```
Query  1    FMEPVKRTEAPGYEYEVIRSPM  21
          FMEPVK+ EAPGY+VIR  PM
Sbjct  712  FMEPVKKNEAPGY+QVIRFPM  732
```

>**emb|CAF99403.1|** unnamed protein product [Tetraodon nigroviridis]
Length=701

Score = 59.6 bits (133), Expect = 4e-08
Identities = 17/21 (80%), Positives = 19/21 (90%), Gaps = 0/21 (0%)

```
Query  1    FMEPVKRTEAPGYEYEVIRSPM  21
          FMEPVK+TEAPGY+  IR  PM
Sbjct  617  FMEPVKKTEAPGY+QAIRFPM  637
```


>**pdb|3D7C|A**  Chain A, Crystal Structure Of The Bromodomain Of Human Gcn5, The General Control Of Amino-Acid Synthesis Protein 5-Like 2

pdb|3D7C|B  Chain B, Crystal Structure Of The Bromodomain Of Human Gcn5, The General Control Of Amino-Acid Synthesis Protein 5-Like 2

Length=112

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

Query 1 FMEPVKRTEAPGYEYEVIRSP 20
FMEPVK++EAP YYEVIR P
Sbjct 28 FMEPVKKSEAPDYEYEVIRFP 47

>ref|XP_001495139.2|  PREDICTED: similar to GCN5 general control of amino-acid synthesis 5-like 2 [Equus caballus]
Length=836

GENE ID: 100053057 LOC100053057 | similar to GCN5 general control of amino-acid synthesis 5-like 2 [Equus caballus]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSP 20
FMEPVK++EAP YYEVIR P
Sbjct 752 FMEPVKKSEAPDYEYEVIRFP 771

>ref|XP_001922732.1|  PREDICTED: im:7156024 [Danio rerio]
Length=795

GENE ID: 555517 kat2a | K(lysine) acetyltransferase 2A [Danio rerio]
(10 or fewer PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSP 20
FMEPVK++EAP YYEVIR P
Sbjct 711 FMEPVKKSEAPDYEYEVIRFP 730

>gb|EDL02540.1|  GCN5 general control of amino acid synthesis-like 2 (yeast), isoform CRA_c [Mus musculus]
Length=481

GENE ID: 14534 Kat2a | K(lysine) acetyltransferase 2A [Mus musculus]
(Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSP 20
FMEPVK++EAP YYEVIR P
Sbjct 397 FMEPVKKSEAPDYEYEVIRFP 416

>gb|EDL02538.1|  GCN5 general control of amino acid synthesis-like 2 (yeast), isoform CRA_a [Mus musculus]
Length=845

GENE ID: 14534 Kat2a | K(lysine) acetyltransferase 2A [Mus musculus]
(Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


Query 1 FMEPVKRTEAPGYEYEVIRSP 20
FMEPVK++EAP YYEVIR P
Sbjct 761 FMEPVKKSEAPDYEYEVIRFP 780

>gb|EAW60801.1|  GCN5 general control of amino-acid synthesis 5-like 2 (yeast), isoform CRA_a [Homo sapiens]
Length=477

GENE ID: 2648 KAT2A | K(lysine) acetyltransferase 2A [Homo sapiens]
(Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVK RTEAPGYYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 393  FMEPVKKSEAPDYEVIRFP 412
```

>**gb|EAW60802.1** |  GCN5 general control of amino-acid synthesis 5-like 2 (yeast), isoform CRA_b [Homo sapiens]
Length=838

GENE ID: 2648 KAT2A | K(lysine) acetyltransferase 2A [Homo sapiens]
(Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVK RTEAPGYYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 754  FMEPVKKSEAPDYEVIRFP 773
```

>**ref|XP_511500.2** |  PREDICTED: GCN5 general control of amino-acid synthesis 5-2 isoform 2 [Pan troglodytes]
Length=837

GENE ID: 454677 KAT2A | K(lysine) acetyltransferase 2A [Pan troglodytes]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)



```
Query 1    FMEPVK RTEAPGYYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 753  FMEPVKKSEAPDYEVIRFP 772
```

>**ref|XP_001166738.1** |  PREDICTED: GCN5 general control of amino-acid synthesis 2 isoform 1 [Pan troglodytes]
Length=852

GENE ID: 454677 KAT2A | K(lysine) acetyltransferase 2A [Pan troglodytes]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVK RTEAPGYYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 768  FMEPVKKSEAPDYEVIRFP 787
```

>**ref|NP_001100520.1** |  general control of amino acid synthesis 5-like 2 [Rattus
gb|EDM06059.1 |  GCN5 general control of amino acid synthesis-like 2 (yeast) (p [Rattus norvegicus]
Length=832

GENE ID: 303539 Gcn512 | GCN5 general control of amino acid synthesis-like 2 (yeast) [Rattus norvegicus]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

```
Query 1    FMEPVK RTEAPGYYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 748  FMEPVKKSEAPDYEVIRFP 767
```


>**ref|XP_001094333.1** |  PREDICTED: similar to GCN5 general control of amino-acid synthesis 5-like 2 [Macaca mulatta]
Length=608

GENE ID: 706004 LOC706004 | similar to GCN5 general control of amino-acid synthesis 5-like 2 [Macaca mulatta]

Score = 54.9 bits (122), Expect = 1e-06


Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

```
Query 1    FMEPVKRTEAPGYEEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 524  FMEPVKKSEAPDYEEVIRFP 543
```

>**gb|AAR03834.1|**  general control of amino-acid synthesis 5-like 2 [Sus scrofa]
Length=117

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVKRTEAPGYEEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 33   FMEPVKKSEAPDYEEVIRFP 52
```

>**gb|AAH03983.1|**  Kat2a protein [Mus musculus]
Length=116

GENE ID: 14534 Kat2a | K(lysine) acetyltransferase 2A [Mus musculus]
(Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

```
Query 1    FMEPVKRTEAPGYEEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 32   FMEPVKKSEAPDYEEVIRFP 51
```

>**pdb|1F68|A**  Chain A, Nmr Solution Structure Of The Bromodomain From Human Gcn5
Length=103

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVKRTEAPGYEEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 24   FMEPVKKSEAPDYEEVIRFP 43
```

>**gb|AAC50641.1|**  GCN5 [Homo sapiens]
Length=476

GENE ID: 2648 KAT2A | K(lysine) acetyltransferase 2A [Homo sapiens]
(Over 10 PubMed links)

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVKRTEAPGYEEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 392  FMEPVKKSEAPDYEEVIRFP 411
```

>**ref|XP_860469.1|**  PREDICTED: similar to GCN5 general control of amino-acid s
5-like 2 isoform 7 [Canis familiaris]
Length=831

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVKRTEAPGYEEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 747  FMEPVKKSEAPDYEEVIRFP 766
```

>**ref|XP_860436.1|**  PREDICTED: similar to General control of amino acid synthe
protein 5-like 2 (Histone acetyltransferase GCN5) (mmGCN5)
isoform 6 [Canis familiaris]
Length=843

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVKRTEAPGYEYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 759  FMEPVKKSEAPDYEVIRFP 778
```

>**ref|XP_860364.1|**  PREDICTED: similar to GCN5 general control of amino-acid s
5-like 2 isoform 4 [Canis familiaris]
Length=584

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVKRTEAPGYEYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 500  FMEPVKKSEAPDYEVIRFP 519
```

>**ref|XP_860401.1|**  PREDICTED: similar to GCN5 general control of amino-acid syn
5-like 2 isoform 5 [Canis familiaris]
Length=834

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)


```
Query 1    FMEPVKRTEAPGYEYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 750  FMEPVKKSEAPDYEVIRFP 769
```

>**ref|XP_849978.1|**  PREDICTED: similar to GCN5 general control of amino-acid s
5-like 2 isoform 2 [Canis familiaris]
Length=844

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

```
Query 1    FMEPVKRTEAPGYEYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 760  FMEPVKKSEAPDYEVIRFP 779
```

>**ref|XP_548094.2|**  PREDICTED: similar to GCN5 general control of amino-acid s
5-like 2 isoform 1 [Canis familiaris]
Length=837

GENE ID: 490971 KAT2A | K(lysine) acetyltransferase 2A [Canis lupus familiaris]

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

```
Query 1    FMEPVKRTEAPGYEYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 753  FMEPVKKSEAPDYEVIRFP 772
```

>**gb|AAB50690.1|** hGCN5=transcriptional adaptor [human, testis, Peptide, 427 aa]
Length=427

Score = 54.9 bits (122), Expect = 1e-06
Identities = 16/20 (80%), Positives = 18/20 (90%), Gaps = 0/20 (0%)

```
Query 1    FMEPVKRTEAPGYEYEVIRSP 20
          FMEPVK++EAP YYEVIR P
Sbjct 343  FMEPVKKSEAPDYEVIRFP 362
```